

SEQUENCE LISTING

<110> Laus, Reiner
Vidovic, Damir
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<120> Compositions and Methods for Dendritic
Cell-Based Immunotherapy

<130> 7636-0022.30

<140> Not Yet Assigned
<141> Filed Herewith

<150> US 60/193,504

<151> 2000-03-30

<160> 30

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 555
<212> PRT
<213> Artificial Sequence

<220>

<223> HER500 construct

<400> 1

Met Arg Ala Ala Pro Leu Leu Leu Ala Arg Ala Ala Ser Leu Ser Leu
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Gly Phe Leu Phe Leu Leu Phe Phe Trp Leu Asp Arg Ser Val Leu Ala
20 25 30
Lys Glu Leu Ala Arg Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr
35 40 45
Asp Met Lys Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met
50 55 60
Leu Arg His Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu
65 70 75 80
Leu Thr Tyr Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile
85 90 95
Gln Glu Val Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln
100 105 110
Val Pro Leu Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu
115 120 125
Asp Asn Tyr Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn
130 135 140
Thr Thr Pro Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln
145 150 155 160
Leu Arg Ser Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg
165 170 175
Asn Pro Gln Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe
180 185 190
His Lys Asn Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser

195	200	205
Arg Ala Cys His Pro Cys Ser	Pro Met Cys Lys Gly Ser Arg Cys Trp	
210	215	220
Gly Glu Ser Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala		
225	230	235
Gly Gly Cys Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His		240
245	250	255
Glu Gln Cys Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu		
260	265	270
Ala Cys Leu His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro		
275	280	285
Ala Leu Val Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro		
290	295	300
Glu Gly Arg Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr		
305	310	315
Asn Tyr Leu Ser Thr Asp Val Gly Ser Gly Ala Gly Met Val His		320
325	330	335
His Arg His Arg Ser Ser Ser Thr Arg Ser Gly Gly Asp Leu Thr		
340	345	350
Leu Gly Leu Glu Pro Ser Glu Glu Ala Pro Arg Ser Pro Leu Ala		
355	360	365
Pro Ser Glu Gly Ala Gly Ser Asp Val Phe Asp Gly Asp Leu Gly Met		
370	375	380
Gly Ala Ala Lys Gly Leu Gln Ser Leu Pro Thr His Asp Pro Ser Pro		
385	390	395
Leu Gln Arg Tyr Ser Glu Asp Pro Thr Val Pro Leu Pro Ser Glu Thr		400
405	410	415
Asp Gly Tyr Val Ala Pro Leu Thr Cys Ser Pro Gln Pro Glu Tyr Val		
420	425	430
Asn Gln Pro Asp Val Arg Pro Gln Pro Pro Ser Pro Arg Glu Gly Pro		
435	440	445
Leu Pro Ala Ala Arg Pro Ala Gly Ala Thr Leu Glu Arg Ala Lys Thr		
450	455	460
Leu Ser Pro Gly Lys Asn Gly Val Val Lys Asp Val Phe Ala Phe Gly		
465	470	475
Gly Ala Val Glu Asn Pro Glu Tyr Leu Thr Pro Gln Gly Gly Ala Ala		
485	490	495
Pro Gln Pro His Pro Pro Pro Ala Phe Ser Pro Ala Phe Asp Asn Leu		
500	505	510
Tyr Tyr Trp Asp Gln Asp Pro Pro Glu Arg Gly Ala Pro Pro Ser Thr		
515	520	525
Phe Lys Gly Thr Pro Thr Ala Glu Asn Pro Glu Tyr Leu Gly Leu Asp		
530	535	540
Val Pro Ala Ala Ala His His His His His		
545	550	555

<210> 2
 <211> 690
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HER500-hGM-CSF construct

<400> 2
 Met Arg Ala Ala Pro Leu Leu Leu Ala Arg Ala Ala Ser Leu Ser Leu
 1 5 10 15

Gly Phe Leu Phe Leu Leu Phe Phe Trp Leu Asp Arg Ser Val Leu Ala
 20 25 30
 Lys Glu Leu Ala Arg Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr
 35 40 45
 Asp Met Lys Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met
 50 55 60
 Leu Arg His Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu
 65 70 75 80
 Leu Thr Tyr Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile
 85 90 95
 Gln Glu Val Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln
 100 105 110
 Val Pro Leu Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu
 115 120 125
 Asp Asn Tyr Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn
 130 135 140
 Thr Thr Pro Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln
 145 150 155 160
 Leu Arg Ser Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg
 165 170 175
 Asn Pro Gln Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe
 180 185 190
 His Lys Asn Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser
 195 200 205
 Arg Ala Cys His Pro Cys Ser Pro Met Cys Lys Gly Ser Arg Cys Trp
 210 215 220
 Gly Glu Ser Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala
 225 230 235 240
 Gly Gly Cys Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His
 245 250 255
 Glu Gln Cys Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu
 260 265 270
 Ala Cys Leu His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro
 275 280 285
 Ala Leu Val Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro
 290 295 300
 Glu Gly Arg Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr
 305 310 315 320
 Asn Tyr Leu Ser Thr Asp Val Gly Ser Gly Ala Gly Gly Met Val His
 325 330 335
 His Arg His Arg Ser Ser Ser Thr Arg Ser Gly Gly Asp Leu Thr
 340 345 350
 Leu Gly Leu Glu Pro Ser Glu Glu Ala Pro Arg Ser Pro Leu Ala
 355 360 365
 Pro Ser Glu Gly Ala Gly Ser Asp Val Phe Asp Gly Asp Leu Gly Met
 370 375 380
 Gly Ala Ala Lys Gly Leu Gln Ser Leu Pro Thr His Asp Pro Ser Pro
 385 390 395 400
 Leu Gln Arg Tyr Ser Glu Asp Pro Thr Val Pro Leu Pro Ser Glu Thr
 405 410 415
 Asp Gly Tyr Val Ala Pro Leu Thr Cys Ser Pro Gln Pro Glu Tyr Val
 420 425 430
 Asn Gln Pro Asp Val Arg Pro Gln Pro Pro Ser Pro Arg Glu Gly Pro
 435 440 445
 Leu Pro Ala Ala Arg Pro Ala Gly Ala Thr Leu Glu Arg Ala Lys Thr
 450 455 460
 Leu Ser Pro Gly Lys Asn Gly Val Val Lys Asp Val Phe Ala Phe Gly

465	470	475	480
Gly Ala Val Glu Asn Pro Glu Tyr Leu Thr Pro Gln Gly Gly Ala Ala			
485	490	495	
Pro Gln Pro His Pro Pro Pro Ala Phe Ser Pro Ala Phe Asp Asn Leu			
500	505	510	
Tyr Tyr Trp Asp Gln Asp Pro Pro Glu Arg Gly Ala Pro Pro Ser Thr			
515	520	525	
Phe Lys Gly Thr Pro Thr Ala Glu Asn Pro Glu Tyr Leu Gly Leu Asp			
530	535	540	
Val Pro Ala Ala Ala Pro Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro			
545	550	555	560
Trp Glu His Val Asn Ala Ile Gln Glu Ala Arg Arg Leu Leu Asn Leu			
565	570	575	
Ser Arg Asp Thr Ala Ala Glu Met Asn Glu Thr Val Glu Val Ile Ser			
580	585	590	
Glu Met Phe Asp Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg Leu Glu			
595	600	605	
Leu Tyr Lys Gln Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro			
610	615	620	
Leu Thr Met Met Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro			
625	630	635	640
Glu Thr Ser Cys Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu			
645	650	655	
Asn Leu Lys Asp Phe Leu Leu Val Ile Pro Phe Asp Cys Trp Glu Pro			
660	665	670	
Val Gln Glu Gly Ala Pro Pro Pro Ala Ala Ala His His His His			
675	680	685	
His His			
690			

<210> 3
 <211> 564
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HER500* construct

<400> 3
 Met Arg Ala Ala Pro Leu Leu Ala Arg Ala Ala Ser Leu Ser Leu
 1 5 10 15
 Gly Phe Leu Phe Leu Leu Phe Phe Trp Leu Asp Arg Ser Val Leu Ala
 20 25 30
 Lys Glu Leu Ala Arg Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr
 35 40 45
 Asp Met Lys Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met
 50 55 60
 Leu Arg His Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu
 65 70 75 80
 Leu Thr Tyr Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile
 85 90 95
 Gln Glu Val Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln
 100 105 110
 Val Pro Leu Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu
 115 120 125
 Asp Asn Tyr Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn
 130 135 140

Thr Thr Pro Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln
 145 150 155 160
 Leu Arg Ser Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg
 165 170 175
 Asn Pro Gln Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe
 180 185 190
 His Lys Asn Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser
 195 200 205
 Arg Ala Cys His Pro Cys Ser Pro Met Cys Lys Gly Ser Arg Cys Trp
 210 215 220
 Gly Glu Ser Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala
 225 230 235 240
 Gly Gly Cys Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His
 245 250 255
 Glu Gln Cys Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu
 260 265 270
 Ala Cys Leu His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro
 275 280 285
 Ala Leu Val Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro
 290 295 300
 Glu Gly Arg Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr
 305 310 315 320
 Asn Tyr Leu Ser Thr Asp Val Gly Ser Ala Ser Ile Ile Asn Phe Glu
 325 330 335
 Lys Leu Gly Ala Gly Gly Met Val His His Arg His Arg Ser Ser Ser
 340 345 350
 Thr Arg Ser Gly Gly Gly Asp Leu Thr Leu Gly Leu Glu Pro Ser Glu
 355 360 365
 Glu Glu Ala Pro Arg Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly Ser
 370 375 380
 Asp Val Phe Asp Gly Asp Leu Gly Met Gly Ala Ala Lys Gly Leu Gln
 385 390 395 400
 Ser Leu Pro Thr His Asp Pro Ser Pro Leu Gln Arg Tyr Ser Glu Asp
 405 410 415
 Pro Thr Val Pro Leu Pro Ser Glu Thr Asp Gly Tyr Val Ala Pro Leu
 420 425 430
 Thr Cys Ser Pro Gln Pro Glu Tyr Val Asn Gln Pro Asp Val Arg Pro
 435 440 445
 Gln Pro Pro Ser Pro Arg Glu Gly Pro Leu Pro Ala Ala Arg Pro Ala
 450 455 460
 Gly Ala Thr Leu Glu Arg Ala Lys Thr Leu Ser Pro Gly Lys Asn Gly
 465 470 475 480
 Val Val Lys Asp Val Phe Ala Phe Gly Ala Val Glu Asn Pro Glu
 485 490 495
 Tyr Leu Thr Pro Gln Gly Gly Ala Ala Pro Gln Pro His Pro Pro Pro
 500 505 510
 Ala Phe Ser Pro Ala Phe Asp Asn Leu Tyr Tyr Trp Asp Gln Asp Pro
 515 520 525
 Pro Glu Arg Gly Ala Pro Pro Ser Thr Phe Lys Gly Thr Pro Thr Ala
 530 535 540
 Glu Asn Pro Glu Tyr Leu Gly Leu Asp Val Pro Ala Ala Ala His His
 545 550 555 560
 His His His His

<210> 4
 <211> 697

<212> PRT

<213> Artificial Sequence

<220>

<223> HER500*-rGM-CSF construct

<400> 4

Met Arg Ala Ala Pro Leu Leu Leu Ala Arg Ala Ala Ser Leu Ser Leu
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Gly Phe Leu Phe Leu Leu Phe Phe Trp Leu Asp Arg Ser Val Leu Ala
20 25 30
Lys Glu Leu Ala Arg Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr
35 40 45
Asp Met Lys Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met
50 55 60
Leu Arg His Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu
65 70 75 80
Leu Thr Tyr Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile
85 90 95
Gln Glu Val Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln
100 105 110
Val Pro Leu Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu
115 120 125
Asp Asn Tyr Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn
130 135 140
Thr Thr Pro Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln
145 150 155 160
Leu Arg Ser Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg
165 170 175
Asn Pro Gln Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe
180 185 190
His Lys Asn Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser
195 200 205
Arg Ala Cys His Pro Cys Ser Pro Met Cys Lys Gly Ser Arg Cys Trp
210 215 220
Gly Glu Ser Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala
225 230 235 240
Gly Gly Cys Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His
245 250 255
Glu Gln Cys Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu
260 265 270
Ala Cys Leu His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro
275 280 285
Ala Leu Val Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro
290 295 300
Glu Gly Arg Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr
305 310 315 320
Asn Tyr Leu Ser Thr Asp Val Gly Ser Ala Ser Ile Ile Asn Phe Glu
325 330 335
Lys Leu Gly Ala Gly Gly Met Val His His Arg His Arg Ser Ser Ser
340 345 350
Thr Arg Ser Gly Gly Gly Asp Leu Thr Leu Gly Leu Glu Pro Ser Glu
355 360 365
Glu Glu Ala Pro Arg Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly Ser
370 375 380
Asp Val Phe Asp Gly Asp Leu Gly Met Gly Ala Ala Lys Gly Leu Gln
385 390 395 400

Ser Leu Pro Thr His Asp Pro Ser Pro Leu Gln Arg Tyr Ser Glu Asp
 405 410 415
 Pro Thr Val Pro Leu Pro Ser Glu Thr Asp Gly Tyr Val Ala Pro Leu
 420 425 430
 Thr Cys Ser Pro Gln Pro Glu Tyr Val Asn Gln Pro Asp Val Arg Pro
 435 440 445
 Gln Pro Pro Ser Pro Arg Glu Gly Pro Leu Pro Ala Ala Arg Pro Ala
 450 455 460
 Gly Ala Thr Leu Glu Arg Ala Lys Thr Leu Ser Pro Gly Lys Asn Gly
 465 470 475 480
 Val Val Lys Asp Val Phe Ala Phe Gly Gly Ala Val Glu Asn Pro Glu
 485 490 495
 Tyr Leu Thr Pro Gln Gly Gly Ala Ala Pro Gln Pro His Pro Pro Pro
 500 505 510
 Ala Phe Ser Pro Ala Phe Asp Asn Leu Tyr Tyr Trp Asp Gln Asp Pro
 515 520 525
 Pro Glu Arg Gly Ala Pro Pro Ser Thr Phe Lys Gly Thr Pro Thr Ala
 530 535 540
 Glu Asn Pro Glu Tyr Leu Gly Leu Asp Val Pro Ala Ala Ala Pro Thr
 545 550 555 560
 Arg Ser Pro Asn Pro Val Thr Arg Pro Trp Lys His Val Asp Ala Ile
 565 570 575
 Lys Glu Ala Leu Ser Leu Leu Asn Asp Met Arg Ala Leu Glu Asn Glu
 580 585 590
 Lys Asn Glu Asp Val Asp Ile Ile Ser Asn Glu Phe Ser Ile Gln Arg
 595 600 605
 Pro Thr Cys Val Gln Thr Arg Leu Lys Leu Tyr Lys Gln Gly Leu Arg
 610 615 620
 Gly Asn Leu Thr Lys Leu Asn Gly Ala Leu Thr Met Ile Ala Ser His
 625 630 635 640
 Tyr Gln Thr Asn Cys Pro Pro Thr Pro Glu Thr Asp Cys Glu Ile Glu
 645 650 655
 Val Thr Thr Phe Glu Asp Phe Ile Lys Asn Leu Lys Gly Phe Leu Phe
 660 665 670
 Asp Ile Pro Phe Asp Cys Trp Lys Pro Val Gln Lys Gly Ala Pro Pro
 675 680 685
 Pro Pro Ala His His His His His
 690 695

<210> 5
 <211> 479
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HER300*-rGM-CSF construct

<400> 5
 Met Arg Ala Ala Pro Leu Leu Ala Arg Ala Ala Ser Leu Ser Leu
 1 5 10 15
 Gly Phe Leu Phe Leu Leu Phe Phe Trp Leu Asp Arg Ser Val Leu Ala
 20 25 30
 Lys Glu Leu Ala Arg Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr
 35 40 45
 Asp Met Lys Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met
 50 55 60
 Leu Arg His Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu

65	70	75	80
Leu	Thr	Tyr	Leu
Pro	Thr	Asn	Ala
Ser	Leu	Ser	Phe
Gln			Leu
			Gln
Gln	Glu	Val	Gln
Gly	Tyr	Val	Leu
Ile	Ala	His	Asn
			Gln
	85	90	95
	100	105	110
Val	Pro	Leu	Gln
Arg	Leu	Arg	Ile
Ile	Val	Arg	Gly
Thr	Gln	Leu	Phe
			Glut
	115	120	125
Asp	Asn	Tyr	Ala
Leu	Ala	Val	Leu
Asp	Asn	Gly	Asp
Pro	Pro	Pro	Leu
Asn	Asn	Asn	Asn
	130	135	140
Thr	Thr	Pro	Val
Thr	Gly	Ala	Ser
Pro	Gly	Gly	Leu
			Arg
	145	150	155
Leu	Arg	Ser	Leu
Thr	Glu	Ile	Leu
Lys	Gly	Gly	Val
			Leu
	165	170	175
Asn	Pro	Gln	Leu
Cys	Tyr	Gln	Asp
Thr	Ile	Leu	Trp
Lys			Lys
	180	185	190
His	Lys	Asn	Asn
Gln	Leu	Ala	Leu
Thr	Thr	Leu	Ile
Asp			Asp
	195	200	205
Arg	Ala	Cys	His
Pro	Cys	Ser	Pro
Met	Cys	Lys	Gly
Ser	Arg	Arg	Cys
			Trp
	210	215	220
Gly	Glu	Ser	Ser
Glu	Asp	Cys	Gln
Ser	Cys	Ser	Leu
Thr			Thr
	225	230	235
Gly	Gly	Cys	Ala
Arg	Cys	Arg	Cys
Lys	Gly	Pro	Leu
			Pro
	245	250	255
Glu	Gln	Cys	Ala
Ala	Ala	Gly	Cys
Thr	Gly	Pro	Lys
			His
	260	265	270
Ala	Cys	Leu	His
Phe	Asn	His	Ser
Gly	Ile	Cys	Glu
			Leu
	275	280	285
Ala	Leu	Val	Thr
Tyr	Asn	Thr	Asp
			Thr
	290	295	300
Glu	Gly	Arg	Tyr
			Thr
	305	310	315
Asn	Tyr	Leu	Ser
Thr	Asp	Val	Gly
Ser	Ala	Ser	Cys
			Val
	325	330	335
Lys	Leu	Ala	Ala
Pro	Thr	Arg	Ser
			Pro
	340	345	350
Lys	His	Val	Asp
Ala	Ile	Lys	Glu
Ala	Leu	Ser	Leu
			Leu
	355	360	365
Arg	Ala	Leu	Glu
Asn	Glu	Lys	Asn
			Glu
	370	375	380
Glu	Phe	Ser	Ile
			Gln
	385	390	395
Tyr	Lys	Gln	Gly
			Leu
	405	410	415
Thr	Met	Ile	Ala
Ser	His	Tyr	Gln
			Thr
	420	425	430
Thr	Asp	Cys	Glu
			Ile
	435	440	445
Leu	Lys	Gly	Phe
Leu	Phe	Leu	Phe
Asp	Ile	Pro	Phe
			Asp
	450	455	460
Gln	Lys	Gly	Ala
Pro	Pro	Pro	Pro
			Ala
	465	470	475

<210> 6
<211> 1665
<212> DNA
<213> Artificial Sequence

<220>

<223> HER500 construct

<400> 6

atgagagctg	cacccctcct	cctggccagg	gcagcaagcc	ttagccttg	tttctgttt	60
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tcgacccaag	tgtgcacccg	cacagacat	aagctgcgc	tccctgccc	tcccagacc	180
cacctggaca	tgctccgcca	cctctaccag	ggctggcagg	tggtgcagg	aaacctggaa	240
ctcacctacc	tgcccaccaa	tgccagcctg	tccttctgc	aggatatcca	ggaggtgcag	300
ggctacgtgc	tcatcgctca	caaccaagt	aggcagg	cactgcagag	gctgcggatt	360
gtgcgaggca	cccagctt	tgaggacaac	tatgccttg	ccgtgt	caatggagac	420
ccgctgaaca	ataccaccc	tgtcacagg	gcctcccc	gaggcctgc	ggagctgcag	480
cttcgaagcc	tcacagagat	cttggaaagga	gggtcttga	tccagcgg	ccccagctc	540
tgctaccagg	acacgattt	gtggaaaggac	atcttccaca	agaacaacca	gctggcttc	600
acactgata	acaccaacc	ctctcg	tgccaccc	gttctccgat	gtgtaaagg	660
tcccgtgt	ggggagagag	ttctgaggat	tgtcagagcc	tgacgcgc	tgtctgt	720
ggtggctgt	cccgctgca	ggggccact	cccactgact	gctgc	gcatgtgt	780
gccggctgca	cgggcc	gactctgac	tgcctgg	gcctcc	caaccacag	840
ggcatctgt	agctgcact	cccagcc	gtcacc	acacagac	gtttgag	900
atgccc	ccgagg	gtatacatt	ggcgc	gactgt	ctgtcc	960
aactac	ctacgg	gggatcgg	gtgtgg	ttgtcc	caggcacc	1020
agctcat	ccagg	gtgg	ctgac	ggctgg	ctctga	1080
gaggcc	gtctcc	actggc	gaagg	gtccgat	atttga	1140
gac	tggggc	ggc	caagg	cttgc	ccccag	1200
ctacagcg	acagt	gggatcgg	gtgtgg	ttgtcc	caggcacc	1260
gcccc	ctgtc	ccagg	cttgc	gtgt	ggccccc	1320
cccc	cccg	gagg	ccct	gtccc	ctgtcg	1380
agg	ctct	ctccc	agg	gtccgat	tttgc	1440
gg	gtgt	ccgt	gg	gtccccc	tttgc	1500
cct	cct	cctg	gtactt	ccccc	tcagccc	1560
gag	ccccc	ccct	actgg	ccccc	ggacc	1620
ggc	ccccc	ccct	ccct	ccccc	ggag	1665
ctgg	ccac	ccat	ggac	ccat	atc	

<210> 7

<211> 2070

<212> DNA

<213> Artificial Sequence

<220>

<223> HER500-hGM-CSF construct

<400> 7

atgagagctg	cacccctcct	cctggccagg	gcagcaagcc	ttagccttg	tttctgttt	60
ctgcttttt	tctggctaga	ccgaagtgt	ctagccaagg	agttggcg	cgggggcc	120
tcgacccaag	tgtgcacccg	cacagacat	aagctgcgc	tccctgccc	tcccagacc	180
cacctggaca	tgctccgcca	cctctaccag	ggctggcagg	tggtgcagg	aaacctggaa	240
ctcacctacc	tgcccaccaa	tgccagcctg	tccttctgc	aggatatcca	ggaggtgcag	300
ggctacgtgc	tcatcgctca	caaccaagt	aggcagg	cactgcagag	gctgcggatt	360
gtgcgaggca	cccagctt	tgaggacaac	tatgccttg	ccgtgt	caatggagac	420
ccgctgaaca	ataccaccc	tgtcacagg	gcctcccc	gaggcctgc	ggagctgcag	480
cttcgaagcc	tcacagagat	cttggaaagga	gggtcttga	tccagcgg	ccccagctc	540
tgctaccagg	acacgattt	gtggaaaggac	atcttccaca	agaacaacca	gctggcttc	600
acactgata	acaccaacc	ctctcg	tgccaccc	gttctccgat	gtgtaaagg	660
tcccgtgt	ggggagagag	ttctgaggat	tgtcagagcc	tgacgcgc	tgtctgt	720
ggtggctgt	cccgctgca	ggggccact	cccactgact	gctgc	gcatgtgt	780
gccggctgca	cgggcc	gactctgac	tgcctgg	gcctcc	caaccacag	840
ggcatctgt	agctgcact	cccagcc	gtcacc	acacagac	gtttgag	900

atgcccata	ccgaggggccg	gtatacattc	ggcgccagct	gtgtgactgc	ctgtccctac	960
aactacctt	ctacggacgt	gggatcgccc	gctggggca	tggccacca	caggcaccgc	1020
agctcatcta	ccaggagttg	cggtggggac	ctgacactag	ggctggagcc	ctctgaagag	1080
gaggccccca	ggtctccact	ggcacccccc	gaaggggctg	gctccgatgt	atttgatgg	1140
gacctggaa	tggggcagc	caaggggctg	caaagccccc	ccacacatga	ccccagccct	1200
ctacagcggt	acagtggaa	ccccacagta	cccctgccc	ctgagactga	tggctacggt	1260
gccccctg	cctgcagccc	ccagcctgaa	tatgtgaacc	agccagatgt	tcggcccccag	1320
cccccttcgc	cccgagaggg	ccctctgcct	gctgcccgc	ctgctggc	cactctggaa	1380
agggccaaga	ctctctcccc	agggagaat	ggggtcgta	aagacgttt	tgccttggg	1440
ggtgcgtgg	agaacccga	gtacttgaca	ccccaggag	gagctgccc	tcagccccac	1500
cctcctcctg	ccttcagccc	agccttcgac	aaccttatt	actgggacca	ggaccacca	1560
gagcgggggg	ctccacccag	cacttcaaa	ggcacaccta	ccgcagagaa	cccagagtac	1620
ctgggtctgg	acgtgccagc	ggccgcaccc	gcccgtcgc	ccagccccag	cacacagccc	1680
tgggagcatg	tgaatgccc	ccaggaggcc	cggcgtctcc	tgaacctgag	tagagacact	1740
gctgctgaga	tgaatgaaac	agtagaagtc	atctcagaaa	tgtttgaccc	ccaggagccg	1800
acctgcctac	agacccgcct	ggagctgtac	aagcagggcc	tgcggggcag	cctcaccaag	1860
ctcaaggggcc	ccttgaccat	gatggccagc	cactacaaac	agcaactgccc	tccaaccccg	1920
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tttctgcttg	tcatccctt	tgactgctgg	gagccagtcc	aggagggcgc	gccacccccc	2040
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<210> 8
<211> 1692
<212> DNA
<213> Artificial Sequence

<220>
<223> HER500* construct

<400> 8						
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<210> 9						
<211> 2091						
<212> DNA						
<213> Artificial Sequence						
<220>						
<223> HER500*-rGM-CSF construct						
<400> 9						
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ccgtccaga	aaggcgcgccc	acccccgg	gcgcatacc	atcaccatca	c	2091
<210> 10						
<211> 1437						
<212> DNA						
<213> Artificial Sequence						
<220>						
<223> HER300*-rGM-CSF construct						
<400> 10						

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atcatctcta	atgagttctc	catccagagg	ccgacatgt	tgcagacccg	cctgaagcta	1200
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agccactacc	agacgaactg	ccctccaacc	ccggaaactg	actgtgaaat	agaagtcacc	1320
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<210> 11
 <211> 32
 <212> PRT
 <213> Homo sapiens

<400> 11
 Met Arg Ala Ala Pro Leu Leu Leu Ala Arg Ala Ala Ser Leu Ser Leu
 1 5 10 15
 Gly Phe Leu Phe Leu Leu Phe Phe Trp Leu Asp Arg Ser Val Leu Ala
 20 25 30

<210> 12
 <211> 3
 <212> PRT
 <213> Homo sapiens

<400> 12
 Lys Glu Leu
 1

<210> 13
 <211> 3
 <212> PRT
 <213> Homo sapiens

<400> 13
 Gly Ala Ala
 1

<210> 14
 <211> 2
 <212> PRT

<213> Artificial Sequence

<220>

<223> linker

<400> 14
Ala Arg
1

<210> 15
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> C-terminal sequence of HER500 and HER500* constructs

<400> 15
Ala Ala Ala His His His His His His
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<210> 16
<211> 15
<212> PRT
<213> Artificial Sequence

<220>

<223> C-terminal sequence of HER500-hGM-CSF construct

<400> 16
Gly Ala Pro Pro Pro Ala Ala Ala His His His His His
1 5 10 15

<210> 17
<211> 13
<212> PRT
<213> Artificial Sequence

<220>

<223> C-terminal sequence of HER500* and HER300* rat GM-CSF constructs

<400> 17
Gly Ala Pro Pro Pro Ala His His His His His
1 5 10

<210> 18
<211> 127
<212> PRT
<213> Homo sapiens

<400> 18
Ala Pro Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp Glu His Val
1 5 10 15
Asn Ala Ile Gln Glu Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp Thr
20 25 30

Ala	Ala	Glu	Met	Asn	Glu	Thr	Val	Glu	Val	Ile	Ser	Glu	Met	Phe	Asp
35							40					45			
Leu	Gln	Glu	Pro	Thr	Cys	Leu	Gln	Thr	Arg	Leu	Glu	Leu	Tyr	Lys	Gln
50						55				60					
Gly	Leu	Arg	Gly	Ser	Leu	Thr	Lys	Leu	Lys	Gly	Pro	Leu	Thr	Met	Met
65					70				75			80			
Ala	Ser	His	Tyr	Lys	Gln	His	Cys	Pro	Pro	Thr	Pro	Glu	Thr	Ser	Cys
85							90					95			
Ala	Thr	Gln	Ile	Ile	Thr	Phe	Glu	Ser	Phe	Lys	Glu	Asn	Leu	Lys	Asp
100						105					110				
Phe	Leu	Leu	Val	Ile	Pro	Phe	Asp	Cys	Trp	Glu	Pro	Val	Gln	Glu	
115						120				125					

<210> 19

<211> 381

<212> DNA

<213> Homo sapiens

<400> 19

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gaagtcatct	cagaaatgtt	tgacctccag	gagccgacct	gcctacagac	ccgcctggag	180
ctgtacaagc	agggcctgcg	gggcagcctc	accaagctca	agggccctt	gaccatgatg	240
gccagccact	acaagcagca	ctgccc	tcca	acccggaaa	cttcctgtgc	300
atcaccttg	aaagttcaa	agagaac	ctg	aaggactt	tgcttgc	360
tgctgggagc	cagtccagga	g			cccccttgac	381

<210> 20

<211> 127

<212> PRT

<213> Rattus norvegicus

<400> 20

Ala	Pro	Thr	Arg	Ser	Pro	Asn	Pro	Val	Thr	Arg	Pro	Trp	Lys	His	Val
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Asp	Ala	Ile	Lys	Glu	Ala	Leu	Ser	Leu	Leu	Asn	Asp	Met	Arg	Ala	Leu
						20			25			30			
Glu	Asn	Glu	Lys	Asn	Glu	Asp	Val	Asp	Ile	Ile	Ser	Asn	Glu	Phe	Ser
						35			40			45			
Ile	Gln	Arg	Pro	Thr	Cys	Val	Gln	Thr	Arg	Leu	Lys	Leu	Tyr	Lys	Gln
						50			55			60			
Gly	Leu	Arg	Gly	Asn	Leu	Thr	Lys	Leu	Asn	Gly	Ala	Leu	Thr	Met	Ile
65						70			75			80			
Ala	Ser	His	Tyr	Gln	Thr	Asn	Cys	Pro	Pro	Thr	Pro	Glu	Thr	Asp	Cys
						85			90			95			
Glu	Ile	Glu	Val	Thr	Thr	Phe	Glu	Asp	Phe	Ile	Lys	Asn	Leu	Lys	Gly
						100			105			110			
Phe	Leu	Phe	Asp	Ile	Pro	Phe	Asp	Cys	Trp	Lys	Pro	Val	Gln	Lys	
						115			120			125			

<210> 21

<211> 381

<212> DNA

<213> Rattus norvegicus

<400> 21

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gaagctctga gcctcctaaa tgacatgcgt gctctggaga acgaaaagaa cgaagacgta	120
gacatcatct ctaatgagtt ctccatccag aggccgacat gtgtgcagac ccgcctgaag	180
ctatacaagc agggctacg gggcaacctc accaaactca atggcgcctt gaccatgata	240
gccagccact accagacgaa ctgcctcca accccggaaa ctgactgtga aatagaagtc	300
accaccttg aggattcat aaagaacctt aaaggcttc tgtttgatat ccctttgac	360
tgctggaagc cggccagaa a	381

<210> 22

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> OVA-derived immunodominant octapeptide

<400> 22

Ser Ile Ile Asn Phe Glu Lys Leu	
1	5

<210> 23

<211> 289

<212> PRT

<213> Homo sapiens

<400> 23

Ser Thr Gln Val Cys Thr Gly Thr Asp Met Lys Leu Arg Leu Pro Ala			
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Ser Pro Glu Thr His Leu Asp Met Leu Arg His Leu Tyr Gln Gly Cys			
20	25	30	
Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr Leu Pro Thr Asn Ala			
35	40	45	
Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val Gln Gly Tyr Val Leu			
50	55	60	
Ile Ala His Asn Gln Val Arg Gln Val Pro Leu Gln Arg Leu Arg Ile			
65	70	75	80
Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr Ala Leu Ala Val Leu			
85	90	95	
Asp Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro Val Thr Gly Ala Ser			
100	105	110	
Pro Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser Leu Thr Glu Ile Leu			
115	120	125	
Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln Leu Cys Tyr Gln Asp			
130	135	140	
Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn Asn Gln Leu Ala Leu			
145	150	155	160
Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys His Pro Cys Ser Pro			
165	170	175	
Met Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser Ser Glu Asp Cys Gln			
180	185	190	
Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys Ala Arg Cys Lys Gly			
195	200	205	
Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys Ala Ala Gly Cys Thr			
210	215	220	
Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu His Phe Asn His Ser			
225	230	235	240
Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val Thr Tyr Asn Thr Asp			
245	250	255	

Thr Phe Glu Ser Met Pro Asn Pro Glu Gly Arg Tyr Thr Phe Gly Ala
 260 265 270
 Ser Cys Val Thr Ala Cys Pro Tyr Asn Tyr Leu Ser Thr Asp Val Gly
 275 280 285
 Ser

<210> 24
 <211> 867
 <212> DNA
 <213> Homo sapiens

<400> 24
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 ctcacccatc tgcccaccaa tgccagcctg tccttcctgc aggatatcca ggaggtgcag 180
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 gtgcgaggca cccagctctt tgaggacaac tatgccttgg ccgtgctaga caatggagac 300
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 ggcacatctgtg agctgcactg cccagccctg gtcacccatc acacagacac gtttgagtcc 780
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 aactaccttt ctacggacgt gggatcc 867

<210> 25
 <211> 217
 <212> PRT
 <213> Homo sapiens

<400> 25
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 Ser Gly Gly Gly Asp Leu Thr Leu Gly Leu Glu Pro Ser Glu Glu Glu
 20 25 30
 Ala Pro Arg Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly Ser Asp Val
 35 40 45
 Phe Asp Gly Asp Leu Gly Met Gly Ala Ala Lys Gly Leu Gln Ser Leu
 50 55 60
 Pro Thr His Asp Pro Ser Pro Leu Gln Arg Tyr Ser Glu Asp Pro Thr
 65 70 75 80
 Val Pro Leu Pro Ser Glu Thr Asp Gly Tyr Val Ala Pro Leu Thr Cys
 85 90 95
 Ser Pro Gln Pro Glu Tyr Val Asn Gln Pro Asp Val Arg Pro Gln Pro
 100 105 110
 Pro Ser Pro Arg Glu Gly Pro Leu Pro Ala Ala Arg Pro Ala Gly Ala
 115 120 125
 Thr Leu Glu Arg Ala Lys Thr Leu Ser Pro Gly Lys Asn Gly Val Val
 130 135 140
 Lys Asp Val Phe Ala Phe Gly Gly Ala Val Glu Asn Pro Glu Tyr Leu
 145 150 155 160
 Thr Pro Gln Gly Gly Ala Ala Pro Gln Pro His Pro Pro Pro Ala Phe
 165 170 175

Ser Pro Ala Phe Asp Asn Leu Tyr Tyr Trp Asp Gln Asp Pro Pro Glu
 180 185 190
 Arg Gly Ala Pro Pro Ser Thr Phe Lys Gly Thr Pro Thr Ala Glu Asn
 195 200 205
 Pro Glu Tyr Leu Gly Leu Asp Val Pro
 210 215

<210> 26
 <211> 651
 <212> DNA
 <213> Homo sapiens

<400> 26
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 tccgaagggg ctggctccga tgtatgtat ggtgacctgg gaatggggc agccaagggg 180
 ctgcaaagcc tccccacaca tgacccagc cctctacagc ggtacagtga ggaccccaca 240
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 gacaacacctt attactggga ccaggaccca ccagagcggg gggctccacc cagcaccttc 600
 aaaggggacac ctacggcaga gaacccagag tacctgggtc tggacgtgccc a 651

<210> 27
 <211> 397
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> NY-ESO-IC tumor antigen

<400> 27
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 1 5 10 15
 Gly Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly
 20 25 30
 Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala
 35 40 45
 Gly Ala Ala Arg Ala Ser Gly Pro Gly Gly Ala Pro Arg Gly Pro
 50 55 60
 His Gly Gly Ala Ala Ser Gly Leu Asn Gly Cys Cys Arg Cys Gly Ala
 65 70 75 80
 Arg Gly Pro Glu Ser Arg Leu Leu Glu Phe Tyr Leu Ala Met Pro Phe
 85 90 95
 Ala Thr Pro Met Glu Ala Glu Leu Ala Arg Arg Ser Leu Ala Gln Asp
 100 105 110
 Ala Pro Pro Leu Pro Val Pro Gly Val Leu Leu Lys Glu Phe Thr Val
 115 120 125
 Ser Gly Asn Ile Leu Thr Ile Arg Leu Thr Ala Ala Asp His Arg Gln
 130 135 140
 Leu Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met
 145 150 155 160
 Trp Ile Thr Gln Cys Phe Leu Pro Val Phe Leu Ala Gln Pro Pro Ser
 165 170 175
 Gly Gln Arg Arg Gly Ala Gly Met Val His His Arg His Arg Ser

180	185	190	
Ser Ser Thr Arg Ser Gly Gly Asp Leu Thr Leu Gly Leu Glu Pro			
195	200	205	
Ser Glu Glu Glu Ala Pro Arg Ser Pro Leu Ala Pro Ser Glu Gly Ala			
210	215	220	
Gly Ser Asp Val Phe Asp Gly Asp Leu Gly Met Gly Ala Ala Lys Gly			
225	230	235	240
Leu Gln Ser Leu Pro Thr His Asp Pro Ser Pro Leu Gln Arg Tyr Ser			
245	250	255	
Glu Asp Pro Thr Val Pro Leu Pro Ser Glu Thr Asp Gly Tyr Val Ala			
260	265	270	
Pro Leu Thr Cys Ser Pro Gln Pro Glu Tyr Val Asn Gln Pro Asp Val			
275	280	285	
Arg Pro Gln Pro Pro Ser Pro Arg Glu Gly Pro Leu Pro Ala Ala Arg			
290	295	300	
Pro Ala Gly Ala Thr Leu Glu Arg Ala Lys Thr Leu Ser Pro Gly Lys			
305	310	315	320
Asn Gly Val Val Lys Asp Val Phe Ala Phe Gly Gly Ala Val Glu Asn			
325	330	335	
Pro Glu Tyr Leu Thr Pro Gln Gly Gly Ala Ala Pro Gln Pro His Pro			
340	345	350	
Pro Pro Ala Phe Ser Pro Ala Phe Asp Asn Leu Tyr Tyr Trp Asp Gln			
355	360	365	
Asp Pro Pro Glu Arg Gly Ala Pro Pro Ser Thr Phe Lys Gly Thr Pro			
370	375	380	
Thr Ala Glu Asn Pro Glu Tyr Leu Gly Leu Asp Val Pro			
385	390	395	

<210> 28

<211> 1191

<212> DNA

<213> Artificial Sequence

<220>

<223> NY-ESO-IC tumor antigen

<400> 28

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ggccggcagag gtccccgggg cgcaggggca gcaagggcct cggggccggg aggagggcgc	180
cccgccgggtc cgcattggcg cgcggcttca gggctgaatg gatgctgcag atgcggggcc	240
agggggccgg agagccgcct gcttgagttc tacctcgcca tgcctttcgc gacaccatg	300
gaagcagagc tggcccgca ggcctggcc caggatccc caccgcttcc cgtgccagg	360
gtgtcttcga aggagttcac tgggtccggc aacatactga ctatccact gactgctgca	420
gaccacggcc aactgcagct ctccatcagc tcctgtctcc agcagcttcc cctgttgatg	480
tggatcacgc agtgctttt gcccgtgtt ttggctcagc ctccctcagg gcagaggcgc	540
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gacctgacac tagggcttga gccctctgaa gaggaggccc ccaggctctcc actggcaccc	660
tccgaagggg ctggctccga tgtatgtat ggtgactgg gaatgggggc agccaagggg	720
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gacaacctct attactggga ccaggaccca ccagagcggg gggctccacc cagcaccc	1140
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<211> 1179
<212> PRT
<213> Artificial Sequence

<220>
<223> SART-3-IC

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35 40 45
Lys Thr Met Gly Pro Ala Trp Asp Gln Gln Glu Glu Gly Val Ser Glu
50 55 60
Ser Asp Gly Asp Glu Tyr Ala Met Ala Ser Ser Ala Glu Ser Ser Pro
65 70 75 80
Gly Glu Tyr Glu Trp Glu Tyr Asp Glu Glu Glu Lys Asn Gln Leu
85 90 95
Glu Ile Glu Arg Leu Glu Gln Leu Ser Ile Asn Val Tyr Asp Tyr
100 105 110
Asn Cys His Val Asp Leu Ile Arg Leu Leu Arg Leu Glu Gly Glu Leu
115 120 125
Thr Lys Val Arg Met Ala Arg Gln Lys Met Ser Glu Ile Phe Pro Leu
130 135 140
Thr Glu Glu Leu Trp Leu Glu Trp Leu His Asp Glu Ile Ser Met Ala
145 150 155 160
Gln Asp Gly Leu Asp Arg Glu His Val Tyr Asp Leu Phe Glu Lys Ala
165 170 175
Val Lys Asp Tyr Ile Cys Pro Asn Ile Trp Leu Glu Tyr Gly Gln Tyr
180 185 190
Ser Val Gly Gly Ile Gly Gln Lys Gly Gly Leu Glu Lys Val Arg Ser
195 200 205
Val Phe Glu Arg Ala Leu Ser Ser Val Gly Leu His Met Thr Lys Gly
210 215 220
Leu Ala Leu Trp Glu Ala Tyr Arg Glu Phe Glu Ser Ala Ile Val Glu
225 230 235 240
Ala Ala Arg Leu Glu Lys Val His Ser Leu Phe Arg Arg Gln Leu Ala
245 250 255
Ile Pro Leu Tyr Asp Met Glu Ala Thr Phe Ala Glu Tyr Glu Glu Trp
260 265 270
Ser Glu Asp Pro Ile Pro Glu Ser Val Ile Gln Asn Tyr Asn Lys Ala
275 280 285
Leu Gln Gln Leu Glu Lys Tyr Lys Pro Tyr Glu Glu Ala Leu Leu Gln
290 295 300
Ala Glu Ala Pro Arg Leu Ala Glu Tyr Gln Ala Tyr Ile Asp Phe Glu
305 310 315 320
Met Lys Ile Gly Asp Pro Ala Arg Ile Gln Leu Ile Phe Glu Arg Ala
325 330 335
Leu Val Glu Asn Cys Leu Val Pro Asp Leu Trp Ile Arg Tyr Ser Gln
340 345 350
Tyr Leu Asp Arg Gln Leu Lys Val Lys Asp Leu Val Leu Ser Val His
355 360 365
Asn Arg Ala Ile Arg Asn Cys Pro Trp Thr Val Ala Leu Trp Ser Arg

370	375	380
Tyr Leu Leu Ala Met Glu Arg His Gly Val Asp His Gln Val Ile Ser		
385	390	395
Val Thr Phe Glu Lys Ala Leu Asn Ala Gly Phe Ile Gln Ala Thr Asp		400
405	410	415
Tyr Val Glu Ile Trp Gln Ala Tyr Leu Asp Tyr Leu Arg Arg Arg Val		
420	425	430
Asp Phe Lys Gln Asp Ser Ser Lys Glu Leu Glu Glu Leu Arg Ala Ala		
435	440	445
Phe Thr Arg Ala Leu Glu Tyr Leu Lys Gln Glu Val Glu Glu Arg Phe		
450	455	460
Asn Glu Ser Gly Asp Pro Ser Cys Val Ile Met Gln Asn Trp Ala Arg		
465	470	475
Ile Glu Ala Arg Leu Cys Asn Asn Met Gln Lys Ala Arg Glu Leu Trp		
485	490	495
Asp Ser Ile Met Thr Arg Gly Asn Ala Lys Tyr Ala Asn Met Trp Leu		
500	505	510
Glu Tyr Tyr Asn Leu Glu Arg Ala His Gly Asp Thr Gln His Cys Arg		
515	520	525
Lys Ala Leu His Arg Ala Val Gln Cys Thr Ser Asp Tyr Pro Glu His		
530	535	540
Val Cys Glu Val Leu Leu Thr Met Glu Arg Thr Glu Gly Ser Leu Glu		
545	550	555
Asp Trp Asp Ile Ala Val Gln Lys Thr Glu Thr Arg Leu Ala Arg Val		
565	570	575
Asn Glu Gln Arg Met Lys Ala Ala Glu Lys Glu Ala Ala Leu Val Gln		
580	585	590
Gln Glu Glu Lys Ala Glu Gln Arg Lys Arg Ala Arg Ala Glu Lys		
595	600	605
Lys Ala Leu Lys Lys Lys Lys Ile Arg Gly Pro Glu Lys Arg Gly		
610	615	620
Ala Asp Glu Asp Asp Glu Lys Glu Trp Gly Asp Asp Glu Glu Glu Gln		
625	630	635
Pro Ser Lys Arg Arg Val Glu Asn Ser Ile Pro Ala Ala Gly Glu		
645	650	655
Thr Gln Asn Val Glu Val Ala Ala Gly Pro Ala Gly Lys Cys Ala Ala		
660	665	670
Val Asp Val Glu Pro Pro Ser Lys Gln Lys Glu Lys Ala Ala Ser Leu		
675	680	685
Lys Arg Asp Met Pro Lys Val Leu His Asp Ser Ser Lys Asp Ser Ile		
690	695	700
Thr Val Phe Val Ser Asn Leu Pro Tyr Ser Met Gln Glu Pro Asp Thr		
705	710	715
Lys Leu Arg Pro Leu Phe Glu Ala Cys Gly Glu Val Val Gln Ile Arg		
725	730	735
Pro Ile Phe Ser Asn Arg Gly Asp Phe Arg Gly Tyr Cys Tyr Val Glu		
740	745	750
Phe Lys Glu Glu Lys Ser Ala Leu Gln Ala Leu Glu Met Asp Arg Lys		
755	760	765
Ser Val Glu Gly Arg Pro Met Phe Val Ser Pro Cys Val Asp Lys Ser		
770	775	780
Lys Asn Pro Asp Phe Lys Val Phe Arg Tyr Ser Thr Ser Leu Glu Lys		
785	790	795
His Lys Leu Phe Ile Ser Gly Leu Pro Phe Ser Cys Thr Lys Glu Glu		
805	810	815
Leu Glu Glu Ile Cys Lys Ala His Gly Thr Val Lys Asp Leu Arg Leu		
820	825	830

Val Thr Asn Arg Ala Gly Lys Pro Lys Gly Leu Ala Tyr Val Glu Tyr
 835 840 845
 Glu Asn Glu Ser Gln Ala Ser Gln Ala Val Met Lys Met Asp Gly Met
 850 855 860
 Thr Ile Lys Glu Asn Ile Ile Lys Val Ala Ile Ser Asn Pro Pro Gln
 865 870 875 880
 Arg Lys Val Pro Glu Lys Pro Glu Thr Arg Lys Ala Pro Gly Gly Pro
 885 890 895
 Met Leu Leu Pro Gln Thr Tyr Gly Ala Arg Gly Lys Gly Arg Thr Gln
 900 905 910
 Leu Ser Leu Leu Pro Arg Ala Leu Gln Arg Pro Ser Ala Ala Ala Pro
 915 920 925
 Gln Ala Glu Asn Gly Pro Ala Ala Ala Pro Ala Val Ala Ala Pro Ala
 930 935 940
 Ala Thr Glu Ala Pro Lys Met Ser Asn Ala Asp Phe Ala Lys Leu Phe
 945 950 955 960
 Leu Arg Gly Ala Gly Gly Met Val His His Arg His Arg Ser Ser Ser
 965 970 975
 Thr Arg Ser Gly Gly Asp Leu Thr Leu Gly Leu Glu Pro Ser Glu
 980 985 990
 Glu Glu Ala Pro Arg Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly Ser
 995 1000 1005
 Asp Val Phe Asp Gly Asp Leu Gly Met Gly Ala Ala Lys Gly Leu Gln
 1010 1015 1020
 Ser Leu Pro Thr His Asp Pro Ser Pro Leu Gln Arg Tyr Ser Glu Asp
 1025 1030 1035 1040
 Pro Thr Val Pro Leu Pro Ser Glu Thr Asp Gly Tyr Val Ala Pro Leu
 1045 1050 1055
 Thr Cys Ser Pro Gln Pro Glu Tyr Val Asn Gln Pro Asp Val Arg Pro
 1060 1065 1070
 Gln Pro Pro Ser Pro Arg Glu Gly Pro Leu Pro Ala Ala Arg Pro Ala
 1075 1080 1085
 Gly Ala Thr Leu Glu Arg Ala Lys Thr Leu Ser Pro Gly Lys Asn Gly
 1090 1095 1100
 Val Val Lys Asp Val Phe Ala Phe Gly Gly Ala Val Glu Asn Pro Glu
 1105 1110 1115 1120
 Tyr Leu Thr Pro Gln Gly Gly Ala Ala Pro Gln Pro His Pro Pro Pro
 1125 1130 1135
 Ala Phe Ser Pro Ala Phe Asp Asn Leu Tyr Tyr Trp Asp Gln Asp Pro
 1140 1145 1150
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> SART-3-IC

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60
 120
 180

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ctggaggagc	agttgtctat	caacgtctat	gactacaact	gccatgtgga	cttgatcaga	360
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caggatggcc	tggacagaga	gcacgtgtat	gaccttttgc	agaaagccgt	gaaggattac	540
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ccgc	cagccacc	ggcacca	atgtcc	ccgat	caagct	2880
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cccac	ccctgc	tga	ggctac	ccccc	ctgc	3180
cagc	gtat	gacca	ccgc	ccc	ccg	3240
cctc	ctgccc	tgctgg	actct	cc	cc	3300
gga	gggtcg	caa	ggc	ccaa	gt	3360
tact	ccca	agac	ttt	gg	cc	3420
gc	cccagg	agg	ctgccc	acc	ctc	3480
ac	ac	ctt	ctgg	acc	cc	3537
ct	cc	at	gg	g	cg	